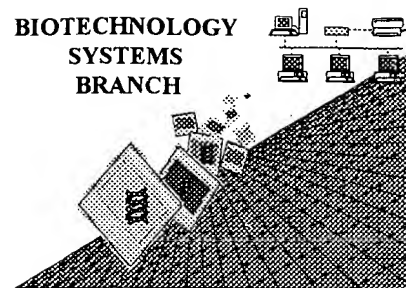


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



#2

0260

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/853,684

Art Unit / Team No. : Team 8

Date Processed by STIC: 7/10/97

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

SEQUENCE LISTING

(1) GENERAL INFORMATION: ^{insert} ~~colon~~

(i) APPLICANT: DEEN, KEITH C
YOUNG, PETER R

(ii) TITLE OF ~~THE~~ INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR, TR6

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: RATNER & PRESTIA
- (B) STREET: P.O. BOX 980
- (C) CITY: VALLEY FORGE
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19482

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: TO BE ASSIGNED
- (B) FILING DATE: 09-MAY-1997
- (C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/041,230
- (B) FILING DATE: 14-MAR-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: PRESTIA, PAUL F.
- (B) REGISTRATION NUMBER: 23,031
- (C) REFERENCE/DOCKET NUMBER: GH-50008

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-407-0700
- (B) TELEFAX: 610-407-0701
- (C) TELEX: 846169

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3,881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

08/853,684 From 8
7/10/97

more throughout
Does Not Comply
Corrected Diskette Needed

#2 YL

10/2

do not use comma

CTTTGCGCCC ACAAATACA CCGACGATGC CCGATCTACT TTAAGGGCTG AAACCCACGG

60 GCCTGAGA

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Arg | Gly | Gln | Asn | Ala | Pro | Ala | Ala | Ser | Gly | Ala | Arg | Lys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | His | Gly | Pro | Gly | Pro | Arg | Glu | Ala | Arg | Gly | Ala | Arg | Pro | Gly | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Val | Pro | Lys | Thr | Leu | Val | Leu | Val | Val | Ala | Ala | Val | Leu | Leu | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Ser | Ala | Glu | Ser | Ala | Leu | Ile | Thr | Gln | Gln | Asp | Leu | Ala | Pro | Gln |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gln | Arg | Ala | Ala | Pro | Gln | Gln | Lys | Arg | Ser | Ser | Pro | Ser | Glu | Gly | Leu |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 |
| Cys | Pro | Pro | Gly | His | His | Ile | Ser | Glu | Asp | Gly | Arg | Asp | Cys | Ile | Ser |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Cys | Lys | Tyr | Gly | Gln | Asp | Tyr | Ser | Thr | Gln | Trp | Asn | Asp | Leu | Leu | Phe |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Cys | Leu | Arg | Cys | Thr | Arg | Cys | Asp | Ser | Gly | Glu | Val | Glu | Leu | Ser | Pro |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Cys | Thr | Thr | Thr | Arg | Asn | Thr | Val | Cys | Gln | Cys | Glu | Glu | Gly | Thr | Phe |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Arg | Glu | Glu | Asp | Ser | Pro | Glu | Met | Cys | Arg | Lys | Cys | Arg | Thr | Gly | Cys |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 |
| Pro | Arg | Gly | Met | Val | Lys | Val | Gly | Asp | Cys | Thr | Pro | Trp | Ser | Asp | Ile |
| | | | | 165 | | | | 170 | | | | | | 175 | |
| Glu | Cys | Val | His | Lys | Glu | Ser | Gly | Ile | Ile | Ile | Gly | Val | Thr | Val | Ala |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ala | Val | Val | Leu | Ile | Val | Ala | Val | Phe | Val | Cys | Lys | Ser | Leu | Leu | Trp |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Lys | Lys | Val | Leu | Pro | Tyr | Leu | Lys | Gly | Ile | Cys | Ser | Gly | Gly | Gly | Gly |
| | 210 | | | | | 215 | | | | 220 | | | | | |
| Asp | Pro | Glu | Arg | Val | Asp | Arg | Ser | Ser | Gln | Arg | Pro | Gly | Ala | Glu | Asp |
| 225 | | | | 230 | | | | | | 235 | | | | | 240 |
| Asn | Val | Leu | Asn | Glu | Ile | Val | Ser | Ile | Leu | Gln | Pro | Thr | Gln | Val | Pro |
| | | | | 245 | | | | 250 | | | | | | 255 | |
| Glu | Gln | Glu | Met | Glu | Val | Gln | Glu | Pro | Ala | Glu | Pro | Thr | Gly | Val | Asn |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Met | Leu | Ser | Pro | Gly | Glu | Ser | Glu | His | Leu | Leu | Glu | Pro | Ala | Glu | Ala |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Glu | Arg | Ser | Gln | Arg | Arg | Arg | Leu | Leu | Val | Pro | Ala | Asn | Glu | Gly | Asp |
| | 290 | | | | | 295 | | | | 300 | | | | | |
| Pro | Thr | Glu | Thr | Leu | Arg | Gln | Cys | Phe | Asp | Asp | Phe | Ala | Asp | Leu | Val |
| 305 | | | | 310 | | | | | | 315 | | | | | 320 |
| Pro | Phe | Asp | Ser | Trp | Glu | Pro | Leu | Met | Arg | Lys | Leu | Gly | Leu | Met | Asp |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Asn | Glu | Ile | Lys | Val | Ala | Lys | Ala | Glu | Ala | Ala | Gly | His | Arg | Asp | Thr |
| | | | 340 | | | | | 345 | | | | | 350 | | |

insert hard return -
bases are all
running on one
line - per 1822(i)
of Sequence Rules,
only 60 bases
PER LINE are
permitted

08/803,684
7/10/97

```

Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
  355                      360                      365
Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
  370                      375                      380
Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
  385                      390                      395                      400
Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser End
                      405                      410 411

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

ATGACCTCCT TTTCTGCTTG CGCTGCACCA GGTGTGATTC AGGTGAAGTG GAGCTAAGTC      60
CCTGCACCAC GACCAGAAAC ACAGTGTGTC AGTGCGAAGA AGGCACCTTC CGGGAAGAAG      120
ATTCTCCTGA GATGTGCCGG AAGTGCCGCA CAGGGTGTCC CAGAGGGATG GTCAAGGTCG      180
GTGATTGTAC ACCCTGGAGT GACATCGAAT GTGTCCACAA AGAATCAGGC ATCATCATAG      240
GAGTCACAGT TGCAGCCGTA GTCTTGATTG TGGCTGTGTT TGTTTGCAAG TCTTTACTGT      300
GGAAGAAAGT CCTTCCTTAC CTGAAAGGCA TCTGCTCAGG TGGTGGTGGG GACCCTGAGC      360
GTGTGGACAG AAGCTCACAA CGACCTGGGG CTGAGGACAA TGTCCTCAAT GAGATCGTGA      420
GTATCTTGCA GCCCACCAG GTCCCTGAGC AGGAAATGGA AGTCCAGGAG CCAGCAGAGC      480
CAACAGGTGT CAACATGTTG TCCCCCGGGG AGTCAGAGCA TCTGCTGGAA CCGGCAGAAG      540
CTGAAAGGTC TCAGAGGAGG AGGCTGCTGG TTCCAGCAAA TGAAGGTGAT CCCACTGAGA      600
CTCTGAGACA GTGCTTCGAT GACTTTGCAG ACTTGGTGCC CTTTGA CTCC TGGGAGCCGC      660
TCATGAGGAA GTTGGGCCTC ATGGACAATG AGATAAAGGT GGCTAAAGCT GAGGCAGCGG      720
GCCACAGGGA CACCTTGTA ACATGCTGA TAAAGTGGGT CAACAAAACC GGGCGAGATG      780
CCTCTGTCCA CACCCTGCTG GATGCCTTGG AGACGCTGGG AGAGAGACTT GCCAAGCAGA      840
AGATTGAGGA CCACTTGTTG AGCTCTGGAA AGTTCATGTA TCTAGAAGGT AATGCAGACT      900
CTGCCATGTC CTAAGTGTGA TTCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT      960
TCTGGAAAAA GCCCAACTGG ACTCCAGTCA GTAGGAAAGT GCCACAATTG TCACATGACC     1020
GGTACTGGAA GAAACTCTCC CATCCAACAT CACCCAGTGG AT                               1062

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val
  1           5           10           15
Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu
  20           25           30
Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys
  35           40           45
Arg Thr Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro
  50           55           60

```

08/853,684
7/10/97

Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly
65 70 75 80
Val Thr Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys
85 90 95
Ser Leu Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser
100 105 110
Gly Gly Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
115 120 125
Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro
130 135 140
Thr Gln Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro
145 150 155 160
Thr Gly Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu
165 170 175
Pro Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
180 185 190
Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe
195 200 205
Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu
210 215 220
Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly
225 230 235 240
His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr
245 250 255
Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu
260 265 270
Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser
275 280 285
Gly Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
290 295 300

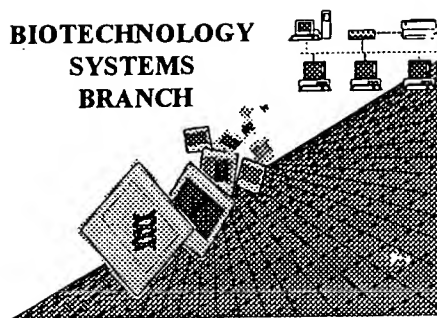
GH-50008

delete

7

GH-50008JHH_i:\skbg\50008/seqlist.txt 1

BIOTECHNOLOGY
SYSTEMS
BRANCH



Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825).

Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested in the following locations:

- 1) Dial-up access to the Patent and Trademark Office Bulletin Board System
Phone Number: 703-305-8950
Cost: Free-of-charge
- 2) Dial-up access through the Internet. FTP site: [ftp.uspto.gov](ftp://ftp.uspto.gov)
Login as "anonymous". The software is in the directory: `/pub/checker`
Cost: Free-of-charge
- 3) For diskette copies, telephone requests to 703-306-2600.
Cost: \$25.00

For Further Information, Contact: Arti Shah at 703-308-4212